

O I P E

SEP 22 2003

PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

<110> Rothschild, Max  
Ciobanu, Dan  
Malek, Massoud  
Plastow, Graham

<120> Novel PRKAG3 Alleles and Use of the Same as Genetic Markers for Reproductive and Meat Quality Traits

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<151> 2000-09-08

<150> 60/260,239  
<151> 2001-01-08

<150> 60/299,111  
<151> 2001-06-18

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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Gly Gly Pro Pro Gly  
35 40 45  
  
ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192  
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Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp			
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Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
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Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
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Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val  
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Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met  
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Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro  
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly  
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Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val  
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Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
130 135 140

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cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser 165 170 175	528
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gcc ctg gtg gcc aac ggc gtc cga gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys 195 200 205	624
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gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe 245 250 255	768
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tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cg <sup>g</sup> aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr	385	390	395	400	1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly	405	410	415		1248
gaa gtc att gac cg <sup>g</sup> att gtc cg <sup>g</sup> gaa cag gtg cac cg <sup>c</sup> ctg gtg ctc Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu	420	425	430		1296
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ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala	450	455	460		1392
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35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
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Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val  
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
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Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met  
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His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser  
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Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe  
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Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys  
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val  
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Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu  
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe  
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val  
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro  
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys  
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr  
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val  
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val  
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr  
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly  
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

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Val	Thr	Thr	Ser	Ser	Glu	Arg	Ser	His	Gly	Asp	Gln	Gly	Asn	Lys	Ala		
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tct	aga	tgg	aca	agg	cag	gag	gat	gta	gag	gaa	ggg	ggg	cct	ccg	ggc		144
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gag	gcc	aca	ttc	ccc	aag	gcc	aca	ccc	ttg	gcc	caa	gcc	gct	ccc	ttg		240
Glu	Ala	Thr	Phe	Pro	Lys	Ala	Thr	Pro	Leu	Ala	Gln	Ala	Ala	Pro	Leu		
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Ala	Glu	Val	Asp	Asn	Pro	Pro	Thr	Glu	Arg	Asp	Ile	Leu	Pro	Ser	Asp		
85					90						95						
tgt	gca	gcc	tca	gcc	tcc	gac	tcc	aac	aca	gac	cat	ctg	gat	ctg	ggc		336
Cys	Ala	Ala	Ser	Ala	Ser	Asp	Ser	Asn	Thr	Asp	His	Leu	Asp	Leu	Gly		
100					105						110						
ata	gag	ttc	tca	gcc	tcg	gcg	tcg	ggg	gat	gag	ctt	ggg	ctg	gtg		384	
Ile	Glu	Phe	Ser	Ala	Ser	Ala	Ala	Ser	Gly	Asp	Glu	Leu	Gly	Leu	Val		
115					120						125						
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Glu	Glu	Lys	Pro	Ala	Pro	Cys	Pro	Ser	Pro	Glu	Val	Leu	Leu	Pro	Arg		
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165							170					175					
aaa	ctg	gtc	atc	ttc	gac	acc	atg	ctg	gag	atc	aag	aag	gcc	ttc	ttt		576
Lys	Leu	Val	Ile	Phe	Asp	Thr	Met	Leu	Glu	Ile	Lys	Lys	Ala	Phe	Phe		
180					185						190						
gcc	ctg	gtg	gcc	aac	ggc	gtc	cga	gca	cct	ttg	tgg	gac	agc	aag		624	
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gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys 290	295	300	912
ttc ctg cac atc ttt ggc acc ctg ctg ccc cgg ccc tcc ttc ctc tac Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr 305	310	315	960
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325	330	335	1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340	345	350	1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355	360	365	1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370	375	380	1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385	390	395	1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405	410	415	1248
gaa gtc att gac cgg att gtc cgg gaa cag gtg cac cgc ctg gtg ctc Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu 420	425	430	1296

gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc		1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile		
435	440	445
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc		1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala		
450	455	460
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga		1452
gccgtggact cagctctcac ttcccctcag ccccacttgc tggctcgct cttgttcagg		1512
taggctccgc ccggggcccc tggcctcagc atcagccct cagtctccct gggcacccag		1572
atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagcattgt		1632
gaaatctacc agcatcaaga ctcactgtgg gaccactgct ttgtcccatt ctcagctgaa		1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac		1752
gtgccttcag gacctccggg gagttagagc tgccctctc cagttcagtt ccccccgtct		1812
gagaatgtcc ctgaaaggaa gccagttaat aaaccttggg tggatggaaat ttggagagtc		1872
g		1873

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 <211> 464  
 <212> PRT  
 <213> Sus scrofa

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Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala			
1	5	10	15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala		
20	25	30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly		
35	40	45

Pro Arg Glu Ser Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln		
50	55	60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu			
65	70	75	80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp		
85	90	95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val  
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met  
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser  
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe  
180 185 190

Ala Leu Val Ala Asn Gly Val Arg Ala Ala Pro Leu Trp Asp Ser Lys  
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val  
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu  
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe  
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val  
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro  
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys  
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr  
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val  
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val  
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr  
 385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly  
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
450 455 460

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<210>    7
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<212> DNA
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Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
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gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96  
 Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
 20 25 30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Gly Pro Pro Gly	144
35 40 45	
ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln	192
50 55 60	
gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu	240
65 70 75 80	
gcc gag gtg gac aac ccc cca aca gag cgg gac atc ctc ccc tct gac Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp	288
85 90 95	
tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly	336
100 105 110	
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val	384
115 120 125	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg	432
130 135 140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met	480
145 150 155 160	
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser	528
165 170 175	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe	576
180 185 190	
gcc ctg gtg gcc aac ggc atc cga gcg gca cct ttg tgg gac agc aag Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys	624
195 200 205	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val	672
210 215 220	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu	720
225 230 235 240	
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe	768
245 250 255	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc	816

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val			
260	265	270	
tac gcc ctc atc aag aac cg <sup>g</sup> atc cac cgc ctg cc <sup>g</sup> gtc ctg gac cct			864
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro			
275	280	285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cg <sup>g</sup> ctt ctc aag			912
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys			
290	295	300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc cg <sup>g</sup> ccc tcc ttc ctc tac			960
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr			
305	310	315	320
cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg			1008
Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val			
325	330	335	
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac			1056
Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp			
340	345	350	
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg			1104
Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val			
355	360	365	
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca			1152
Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr			
370	375	380	
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cg <sup>g</sup> aca			1200
Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr			
385	390	395	400
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg			1248
Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly			
405	410	415	
gaa gtc att gac cg <sup>g</sup> att gtc cg <sup>g</sup> gaa cag gtg cac cgc ctg gtg ctc			1296
Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu			
420	425	430	
gtg gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc			1344
Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile			
435	440	445	
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc			1392
Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala			
450	455	460	
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga			1452
gccgtggact cagctctcac ttcccctcag cccccacttgc tggctggct cttttcagg			1512
taggctccgc ccggggcccc tggcctcagc atcagccccct cagtctccct gggcacccag			1572

atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagccttgt 1632  
gaaatctacc agcatcaaga ctcactgtgg gaccactgct ttgtcccatt ctcagctgaa 1692  
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac 1752  
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt cccccctgct 1812  
gagaatgtcc ctggaaggaa gccagttaat aaaccttgggt tggatggaaat ttggagagtc 1872  
g 1873

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<212> PRT  
<213> Sus scrofa

<400> 8

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
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Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
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Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly  
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val  
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met

145                    150                    155                    160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser  
165                    170                    175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe  
180                    185                    190

Ala Leu Val Ala Asn Gly Ile Arg Ala Ala Pro Leu Trp Asp Ser Lys  
195                    200                    205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val  
210                    215                    220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu  
225                    230                    235                    240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe  
245                    250                    255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val  
260                    265                    270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro  
275                    280                    285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys  
290                    295                    300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr  
305                    310                    315                    320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val  
325                    330                    335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
340                    345                    350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val  
355                    360                    365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
370                    375                    380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr  
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly  
405 410 415

Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile  
435 440 445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
450 455 460

<210> 9  
<211> 1873  
<212> DNA  
<213> Sus scrofa

<220>  
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<222> (1)..(1392)  
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gta acc acc agc tca gaa aga agc cat ggg gac cag ggg aac aag gcc 96  
Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
20 25 30

tct aga tgg aca agg cag gag gat gta gag gaa ggg ggg cct ccg ggc 144  
Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Gly Gly Pro Pro Gly  
35 40 45

ccg agg gaa ggt ccc cag tcc agg cca gtt gct gag tcc acc ggg cag 192  
Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
50 55 60

gag gcc aca ttc ccc aag gcc aca ccc ttg gcc caa gcc gct ccc ttg 240  
Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
65 70 75 80

gcc gag gtg gac aac ccc cca aca gag cggt gac atc ctc ccc tct gac 288  
Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
85 90 95

tgt gca gcc tca gcc tcc gac tcc aac aca gac cat ctg gat ctg ggc		336	
Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly			
100	105	110	
ata gag ttc tca gcc tcg gcg gcg tcg ggg gat gag ctt ggg ctg gtg		384	
Ile Glu Phe Ser Ala Ser Ala Ser Gly Asp Glu Leu Gly Leu Val			
115	120	125	
gaa gag aag cca gcc ccg tgc cca tcc cca gag gtg ctg tta ccc agg		432	
Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg			
130	135	140	
ctg ggc tgg gat gat gag ctg cag aag ccg ggg gcc cag gtc tac atg		480	
Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met			
145	150	155	160
cac ttc atg cag gag cac acc tgc tac gat gcc atg gcg acc agc tcc		528	
His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser			
165	170	175	
aaa ctg gtc atc ttc gac acc atg ctg gag atc aag aag gcc ttc ttt		576	
Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe			
180	185	190	
gcc ctg gtg gcc aac ggc gtc caa gcg gca cct ttg tgg gac agc aag		624	
Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys			
195	200	205	
aag cag agc ttc gtg ggg atg ctg acc atc aca gac ttc atc ttg gtg		672	
Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val			
210	215	220	
ctg cac cgc tat tac agg tcc ccc ctg gtc cag atc tac gag att gaa		720	
Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu			
225	230	235	240
gaa cat aag att gag acc tgg agg gag atc tac ctt caa ggc tgc ttc		768	
Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe			
245	250	255	
aag cct ctg gtc tcc atc tct ccc aat gac agc ctg ttc gaa gct gtc		816	
Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val			
260	265	270	
tac gcc ctc atc aag aac cgg atc cac cgc ctg ccg gtc ctg gac cct		864	
Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro			
275	280	285	
gtc tcc ggg gct gtg ctc cac atc ctc aca cat aag cgg ctt ctc aag		912	
Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys			
290	295	300	
ttc ctg cac atc ttt ggc acc ctg ctg ccc ccg ccc tcc ttc ctc tac		960	
Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr			
305	310	315	320

cgc acc atc caa gat ttg ggc atc ggc aca ttc cga gac ttg gcc gtg Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val 325                   330                   335	1008
gtg ctg gaa acg gcg ccc atc ctg acc gca ctg gac atc ttc gtg gac Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp 340                   345                   350	1056
cgg cgt gtg tct gcg ctg cct gtg gtc aac gaa act gga cag gta gtg Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val 355                   360                   365	1104
ggc ctc tac tct cgc ttt gat gtg atc cac ctg gct gcc caa caa aca Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr 370                   375                   380	1152
tac aac cac ctg gac atg aat gtg gga gaa gcc ctg agg cag cgg aca Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr 385                   390                   395                   400	1200
ctg tgt ctg gaa ggc gtc ctt tcc tgc cag ccc cac gag acc ttg ggg Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly 405                   410                   415	1248
gaa gtc att gac cg <sup>g</sup> att gtc cg <sup>g</sup> gaa cag gtg cac cg <sup>c</sup> ctg gtg ctc Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu 420                   425                   430	1296
tg <sup>g</sup> gat gag acc cag cac ctt ctg ggc gtg gtg tcc ctc tct gac atc Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile 435                   440                   445	1344
ctt cag gct ctg gtg ctc agc cct gct gga att gat gcc ctc ggg gcc Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala 450                   455                   460	1392
tgagaacctt ggaacctttg ctctcaggcc acctggcaca cctggaagcc agtgaaggga	1452
gccgtggact cagctctcac ttccccctcag ccccacttgc tggctggct cttgttcagg	1512
taggctccgc ccggggccccc tgccctcagc atcagccct cagtctccct gggcacccag	1572
atctcagact ggggcaccct gaagatggga gtggcccagc ttatagctga gcagcattgt	1632
gaaatctacc agcatcaaga ctcactgtgg gaccactgct ttgtcccatt ctcagctcaa	1692
atgatggagg gcctcataag aggggtggac agggcctgga gtagaggcca gatcagtgac	1752
gtgccttcag gacctccggg gagttagagc tgccctctct cagttcagtt ccccccgtct	1812
gagaatgtcc ctggaaggaa gccagttaat aaaccttgggt tggatgaaat ttggagagtc	1872
g	1873

<210> 10  
<211> 464

<212> PRT  
<213> Sus scrofa

<400> 10

Met Ser Phe Leu Glu Gln Gly Glu Ser Arg Ser Trp Pro Ser Arg Ala  
1 5 10 15

Val Thr Thr Ser Ser Glu Arg Ser His Gly Asp Gln Gly Asn Lys Ala  
20 25 30

Ser Arg Trp Thr Arg Gln Glu Asp Val Glu Glu Gly Pro Pro Gly  
35 40 45

Pro Arg Glu Gly Pro Gln Ser Arg Pro Val Ala Glu Ser Thr Gly Gln  
50 55 60

Glu Ala Thr Phe Pro Lys Ala Thr Pro Leu Ala Gln Ala Ala Pro Leu  
65 70 75 80

Ala Glu Val Asp Asn Pro Pro Thr Glu Arg Asp Ile Leu Pro Ser Asp  
85 90 95

Cys Ala Ala Ser Ala Ser Asp Ser Asn Thr Asp His Leu Asp Leu Gly  
100 105 110

Ile Glu Phe Ser Ala Ser Ala Ala Ser Gly Asp Glu Leu Gly Leu Val  
115 120 125

Glu Glu Lys Pro Ala Pro Cys Pro Ser Pro Glu Val Leu Leu Pro Arg  
130 135 140

Leu Gly Trp Asp Asp Glu Leu Gln Lys Pro Gly Ala Gln Val Tyr Met  
145 150 155 160

His Phe Met Gln Glu His Thr Cys Tyr Asp Ala Met Ala Thr Ser Ser  
165 170 175

Lys Leu Val Ile Phe Asp Thr Met Leu Glu Ile Lys Lys Ala Phe Phe  
180 185 190

Ala Leu Val Ala Asn Gly Val Gln Ala Ala Pro Leu Trp Asp Ser Lys  
195 200 205

Lys Gln Ser Phe Val Gly Met Leu Thr Ile Thr Asp Phe Ile Leu Val  
210 215 220

Leu His Arg Tyr Tyr Arg Ser Pro Leu Val Gln Ile Tyr Glu Ile Glu  
225 230 235 240

Glu His Lys Ile Glu Thr Trp Arg Glu Ile Tyr Leu Gln Gly Cys Phe  
245 250 255

Lys Pro Leu Val Ser Ile Ser Pro Asn Asp Ser Leu Phe Glu Ala Val  
260 265 270

Tyr Ala Leu Ile Lys Asn Arg Ile His Arg Leu Pro Val Leu Asp Pro  
275 280 285

Val Ser Gly Ala Val Leu His Ile Leu Thr His Lys Arg Leu Leu Lys  
290 295 300

Phe Leu His Ile Phe Gly Thr Leu Leu Pro Arg Pro Ser Phe Leu Tyr  
305 310 315 320

Arg Thr Ile Gln Asp Leu Gly Ile Gly Thr Phe Arg Asp Leu Ala Val  
325 330 335

Val Leu Glu Thr Ala Pro Ile Leu Thr Ala Leu Asp Ile Phe Val Asp  
340 345 350

Arg Arg Val Ser Ala Leu Pro Val Val Asn Glu Thr Gly Gln Val Val  
355 360 365

Gly Leu Tyr Ser Arg Phe Asp Val Ile His Leu Ala Ala Gln Gln Thr  
370 375 380

Tyr Asn His Leu Asp Met Asn Val Gly Glu Ala Leu Arg Gln Arg Thr  
385 390 395 400

Leu Cys Leu Glu Gly Val Leu Ser Cys Gln Pro His Glu Thr Leu Gly  
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Glu Val Ile Asp Arg Ile Val Arg Glu Gln Val His Arg Leu Val Leu  
420 425 430

Val Asp Glu Thr Gln His Leu Leu Gly Val Val Ser Leu Ser Asp Ile

435

440

445

Leu Gln Ala Leu Val Leu Ser Pro Ala Gly Ile Asp Ala Leu Gly Ala  
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